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1632

SAT, Lee  
#8

PAGE:

1

APR 21 2000

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/316,048

DATE: 04/19/2000

TIME: 10:13:02

Input Set: I316048.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: MOULAND, Andrew J.
2      COHEN, Eric A.
3      WICKHAM, Louise
4      LUO, Ming
5      DUCHAINE, Thomas
6  <120> TITLE OF INVENTION: MAMMALIAN STAUFEN AND USE THEREOF
7  <130> FILE REFERENCE: 10875-77
8  <140> CURRENT APPLICATION NUMBER: US/09/316,048
9  <141> CURRENT FILING DATE: 1999-05-21
10 <150> EARLIER APPLICATION NUMBER: CA 2,238,656
11 <151> EARLIER FILING DATE: 1998-05-22
12 <160> NUMBER OF SEQ ID NOS: 27
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16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (3)..(1775)
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24      1          5          10          15
25      ggc ggc tgc ggc tct ctg tgc gct ccc gct tcc ttt gac cgc ctc ccc      95
26      Gly Gly Cys Ala Ala Pro Ala Ser Phe Asp Arg Leu Pro
27      20          25          30
28      ccc ccg gcc ccg cgc ctc ttc      143
29      Pro Pro Ala A Ala Arg Leu Phe
30      35          40          45
31      cct ccc ttc cct tcc ttc ccc      191
32      Pro Pro Phe Ala Ser Phe Pro
33      50          55          60
34      tcc tgc ccg acg agc tgc gag      239
35      Ser Ser Pro Thr Ser Ser Glu
36      65          70          75
37      cag cag cca gaa aat gca ctg tgc      287
38      Gln Gln Pro Glu Ser Ile Asn Ala Leu Cys
39      80          85          90          95
40      atg aaa ctt gga aaa aaa cca atg tat aag cct gtt gac cct tac tct      335
41      Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser
42      100          105          110
43      cgg atg cag tcc acc tat aac tac aac atg aga gga ggt gct tat ccc      383
44      Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro

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*Potential interference*  
*09/286, 959*  
*although I made a*  
*102(b) w/ 1449 Des Grasseillers et al*  
*as evidenced by Wickham*  
*and a 103 on the proteins*

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## RAW SEQUENCE LISTING

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95      Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe
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98      Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp
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100     gag ttc agg atg cct tat cta agt cat cag cag ctg cct gct gga att 1295
101     Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile
102     420                      425                      430
103     ctt ccc atg gtg ccc gag gtc gcc cag gct gta gga gtt agt caa gga 1343
104     Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly
105     435                      440                      445
106     cat cac acc aaa gat ttt acc agg gca gct ccg aat cct gcc aag gcc 1391
107     His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala
108     450                      455                      460
109     acg gta act gcc atg ata gcc cga gag ttg ttg tat ggg ggc acc tcg 1439
110     Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser
111     465                      470                      475
112     ccc aca gcc gag acc att tta aag aat aac atc tct tca ggc cac gta 1487
113     Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val
114     480                      485                      490                      495
115     ccc cat gga cct ctc acg aga ccc tct gag caa ctg gac tat ctt tcc 1535
116     Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser
117     500                      505                      510
118     aga gtc cag gga ttc cag gtt gaa tac aaa gac ttc ccc aaa aac aac 1583
119     Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn
120     515                      520                      525
121     aag aac gaa ttt gta tct ctt atc aat tgc tcc tct cag cca cct ctg 1631
122     Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu
123     530                      535                      540
124     atc agc cat ggt atc ggc aag gat gtg gag tcc tgc cat gat atg gct 1679
125     Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala
126     545                      550                      555
127     gcg ctg aac atc tta aag ttg ctg tct gag ttg gac caa caa agt aca 1727
128     Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr
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130     gag atg cca aga aca gga aac gga cca atg tct gtg tgt ggg agg tgc 1775
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147 cttgaataag tctccacacag ttgtataaat tggacaattt aggaatttta aacttttagat 2675
148 gatcatttgg ttccattttt atttcatttt tatttttgtt aatgcaaaca ggacttaaat 2735
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150 ttgaggactt agctttcact acactacagg atatgatctc catgtagtcc atataaacct 2855
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153 agtgtgtgca ctgaggctct gcgtgtggtc cgtatggaaa acctggtagc cctgcgagtt 3035
154 aagtactgct tccattcatt gtttacgctg gaatttttct ccccatggaa tgtaagtaaa 3095
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158 &lt;212&gt; TYPE: PRT

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160 &lt;400&gt; SEQUENCE: 2

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164 20 25 30
165 Pro Ala Arg Arg Arg Pro Pro Pro Pro Arg Pro Leu Arg Leu Phe Pro
166 35 40 45
167 Pro Phe Val Pro Ser Ser Ser Pro Phe Phe Pro Ser Ser Phe Pro Ser
168 50 55 60
169 Ser Pro Pro Pro Pro Arg Thr Ala Gly Arg Gly Thr Ser Ser Glu Gln
170 65 70 75 80
171 Gln Pro Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys Met
172 85 90 95
173 Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser Arg
174 100 105 110
175 Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro Pro
176 115 120 125
177 Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val Glu
178 130 135 140
179 Leu Ser Val Gly Gly Gln Phe Asn Gly Lys Gly Lys Thr Arg Gln
180 145 150 155 160
181 Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln Asn
182 165 170 175
183 Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu Glu
184 180 185 190
185 Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala Leu
186 195 200 205
187 Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly Pro
188 210 215 220
189 Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe Val
190 225 230 235 240
191 Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala
192 245 250 255
193 Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala Val
194 260 265 270

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198              290                      295                      300
199      Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr Thr
200      305                      310                      315                      320
201      Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met Gln
202              325                      330                      335
203      Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys Lys
204              340                      345                      350
205      Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly Phe
206              355                      360                      365
207      Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu Glu
208              370                      375                      380
209      Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe Phe
210      385                      390                      395                      400
211      Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp Glu
212              405                      410                      415
213      Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile Leu
214              420                      425                      430
215      Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly His
216              435                      440                      445
217      His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala Thr
218              450                      455                      460
219      Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser Pro
220      465                      470                      475                      480
221      Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val Pro
222              485                      490                      495
223      His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser Arg
224              500                      505                      510
225      Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn Lys
226              515                      520                      525
227      Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu Ile
228              530                      535                      540
229      Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala Ala
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231      Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr Glu
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VERIFICATION SUMMARY  
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Line ? Error/Warning

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